

HOMOLOGOUS PROTEINS:

Top BLAST hits:

	Score	E
CRA 180000 05106129 /altid=gi 4557020 /def=ref NP_001289.1 chl...	505	e-141
CRA 180000 05106132 /altid=gi 3121853 /def=sp O15247 CL12_HUMAN ...	504	e-141
CRA 180000 05106119 /altid=gi 7330335 /def=ref NP_039234.1 chlor...	334	3e-90
CRA 180000 05106101 /altid=gi 6685319 /def=sp Q9Y696 CL14_HUMAN ...	334	3e-90
CRA 180000 05106144 /altid=gi 8393147 /def=ref NP_058625.1 chl...	334	3e-90
CRA 180000 05106169 /altid=gi 7304963 /def=ref NP_038913.1 chlor...	333	4e-90
CRA 180000 05106175 /altid=gi 17592636 /def=sp BAA94345.1 (AB035520)...	332	1e-89
CRA 180000 05106120 /altid=gi 6685295 /def=sp Q9Z0W7 CLI4_RAT CH...	330	7e-89
CRA 180000 05106163 /altid=gi 4588534 /def=gb AAD26136.1 AF10919...	328	2e-88
CRA 180000 05106170 /altid=gi 12232044 /def=gb AAG49367.1 AF323...	326	6e-88

BLAST dbEST hits:

	Score	E
gi 3537999 /dataset=dbest /taxon=9606 ...	1063	0.0
gi 10371515 /dataset=dbest /taxon=96...	827	0.0
gi 4630214 /dataset=dbest /taxon=9606 ...	823	0.0
gi 9867186 /dataset=dbest /taxon=960...	646	0.0
gi 1235759 /dataset=dbest /taxon=9606 ...	607	e-171
gi 1235308 /dataset=dbest /taxon=9606 ...	605	e-171
gi 3752728 /dataset=dbest /taxon=9606 ...	543	e-152

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|3537999 uterus

gi|10371515 lung

gi|4630214 germ cell

gi|9867186 liver

gi|1235759 parathyroid gland

gi|1235308 prostate

gi|3752728 placenta

From tissue screening panels:

Whole liver

1 MSGLPEGTQV LPEIELEFVKA GSDGESIGNC PEQWLEMLL WLKGVKENVT
 51 TVDMTRKPER LKDLAPGTNP PELVYNKEIK TDFIKIEEEL EQTLASPPYP
 101 HLSKZYKESF DVGCNLFAPF SAYIKNTQPE ANKNFKESLL YEFKRLDDYL
 151 NTFLLDEIDF DSAEPPVSR RLELDGDQIT LADCSLLEKL NIKVAAKKY
 201 PDEFIPAEPS GWWPYLHNAY AREEFTHTCP EDPEIENTYA NVAKQKS (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDCC00001 PS00001 ASN_GLYCOSYLATION
 N-glycosylation site

48-61 NVTT

[2] PDCC00005 PS00005 PKC_PHOSPHO_SITE
 Protein kinase C phosphorylation site

Number of matches: 4

1	55-57 TRF
2	103-105 SPE
3	127-129 TQK
4	169-171 SKR

[3] PDCC00006 PS00006 CK2_PHOSPHO_SITE
 Casein kinase II phosphorylation site

Number of matches: 7

1	3-11 TVVD
2	21-23 SDGE
3	51-53 TTVD
4	127-130 TQKE
5	162-165 SAGE
6	180-183 TLAD
7	228-231 TQPE

[4] PDCC00007 PS00007 TYR_PHOSPHO_SITE
 Tyrosine kinase phosphorylation site

133-239 PEIENTY

[5] PDCC00008 PS00008 MYRISTYL
 N-myristoylation site

Number of matches: 2

1	3-8 GLRPGT
2	44-49 GVKENV

BLAST Alignment to Top Hit:

ACRA117600005198129 /altid=gi14557620 /def-ref:NP_001230.11 chloride
intracellular channel 2 [Homo sapiens] /org=Homo sapiens
/taxon=9606 /dataset=nraa /length=243
Length = 243

Score = 505 bits (1286), Expect = e-141
Identities = 242/243 (99%), Positives = 242/243 (99%)
Frame = +2

Query: 155 MSGLRPGTQVDPEIELEVKAGSDGESIGNCPFCQRLMILWLKGVKFNVTTVDMTRKPEE 334
MSGLRPGTQVDPEIELEVKAGSDGESIGNCPFCQRLMILWLKGVKFNVTTVDMTRKPEE
Sbjct: 1 MSGLRPGTQVDPEIELEVKAGSDGESIGNCPFCQRLMILWLKGVKFNVTTVDMTRKPEE 60

Query: 335 LFDLAPGTNPFFLVYNFELKTDFFIKIEEFLEQLAPPYPHLSPKYKESFDVGCNLFKAF 514
LFDLAPGTNPFFLVYNFELKTDFFIKIEEFLEQLAPPYPHLSPKYKESFDVGCNLFKAF
Sbjct: 61 LFDLAPGTNPFFLVYNFELKTDFFIKIEEFLEQLAPPYPHLSPKYKESFDVGCNLFKAF 120

Query: 515 SAYIKNTQHEANKNFEKSLLEKFKRLDDYLNTPLLDEIDPDSAEPPVSRFLFDGQQLT 694
SAYIKNTQHEANKNFEKSLLEKFKRLDDYLNTPLLDEIDPDSAEPPVSRFLFDGQQLT
Sbjct: 121 SAYIKNTQHEANKNFEKSLLEKFKRLDDYLNTPLLDEIDPDSAEPPVSRFLFDGQQLT 180

Query: 695 LADCSLLPKLNIKVAANKYRDFDIPAEFSGVWRYLHNAYAREEFTHTCPEEKKEIENTYA 874
LADCSLLPKLNIKVAANKYRDFDIPAEFSGVWRYLHNAYAREEFTHTCPEEKKEIENTYA
Sbjct: 181 LADCSLLPKLNIKVAANKYRDFDIPAEFSGVWRYLHNAYAREEFTHTCPEEKKEIENTYA 240

Query: 875 N/A 883
N/A

Sbjct: 241 N/A 243 (SEQ ID NO:4)

1 AGAAGTAATC ATGGTTCCCTG ATAAGACGG CAAAACAGC AAGTGATCT
51 TTCCAGTCCA AG TTCCAAG AAAAAGAGAA CTA GT T C CACA TAAA
101 AAGTCCCGAG ACTCAACCAG GCGGTCAGC ATTCCCTCT TGTAGAGAG
151 AGTGAAGATT GCAACCCAGA ACAAAATCT GCGTCTCTA GCAGIAGGAT
201 TGAGGTGGA AATATTAAAT GAAATATAAT CTCTTAA TCCTTTAGAG
251 AGIATCAGTG AATAACATCT CTCTTCAATA AAAAAATTC AAGTATCTC
301 TGCTCTCTCT CTCTGAAATC CTCTCAATCT AAAAAATTC CAATAAGAG
351 CCGTCTTTCTG CTCTAGAGAG CCACTCTCA AAAAAATTC CTAAAGAGAG
401 TCTGCTCTCT TTATATATA GAACTAGCA CTCTATCTCT GTCTCTCTCT
451 GCATCTCTCT CTCTCTCTCT GATCTAGCT ATCTAAATCT CTCTGAGAG
501 ACCCTCAATC TTCTAGAGAG GAACTTAAIA AAAAAATTC TCGTCTCTCT
551 TTGATTTAAA TCTTAGAGAG CCAAGAGAGAG AAAAAATTC TCAAGAGAG
601 GCATTTAAAT AATTAGAGAG TTCTCTCTCT CACTCTCTCT GAGAGAGAG
651 TGCTCTCTCT TCTCTAGAG TCTCTAGAG TTCTCTCTCT CTCTCTCTCT
701 CACTAAATCT AATCTAGAG TCTCTAGAG TCTCTCTCT CTCTCTCTCT
751 TATCTCTCT TCTCTAGAG GCACTAGAG TCTCTCTCT AGATCTAGAG
801 AAGATCTCT GCTCTCTCT CCGTCTCTCT GCTCTCTCT AGATCTAGAG
851 TTCTCTCTCT GCTCTCTCT CACTCTCTCT AATCTCTCT AGATCTATCT
901 AATCTCTCT AATCTCTCT AATCTCTCT AAAAAATTC AATCTCTCT
951 TAGATCTCT AAAAAATTC CTCTCTCT TCTCTCTCT AATCTCTCT
1001 GATCTCTCT GCTCTCTCT CTCTCTCT AAAAAATTC AATCTCTCT
1051 CTCTCTCTCT AAAAAATTC ATCTCTCTCT AAAAAATTC AATCTCTCT
1101 ACTCTCTCT CAAATCTCT TCTCTCTCT TCTCTCTCT AATCTCTCT
1151 AATCTCTCT TCTCTCTCT CACTCTCTCT AAAAAATTC AATCTCTCT
1201 GCACTCTCT AATCTCTCT AAAAAATTC AAAAAATTC AAAAAATTC
1251 TATCTCTCT GCTCTCTCT GCTCTCTCT TCTCTCTCT AAAAAATTC
1301 TGCTCTCTCT AATCTCTCT CCACTCTCT CCACTCTCT CTCTCTCTCT
1351 TTCTCTCTCT GCACTCTCT AAAAAATTC CCACTCTCT CTCTCTCTCT
1401 AAAAAATTC GCTCTCTCT TCTCTCTCT AGCTCTCTCT CATTCTCTCT
1451 TCTCTCTCT TCTCTCTCT GCTCTCTCT CATTCTCTCT TCTCTCTCT
1501 TAACTCTCT AATCTCTCT AAAAAATTC AAAAAATTC TAACTCTCT
1551 GAACTCTCT TCTCTCTCT AATCTCTCT TAACTCTCT AAAAAATTC
1601 TCTCTCTCT CCACTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
1651 TCTCTCTCT CCACTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
1701 TAACTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
1751 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
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1951 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
2001 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
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2101 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
2151 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
2201 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
2251 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
2301 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
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3001 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
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3101 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
3151 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
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4001 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
4051 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT
4101 TCTCTCTCT TCTCTCTCT TAACTCTCT TAACTCTCT TCTCTCTCT

FIGURE 3, page 1 of 24

3151 ATGAAATAAT CTTAATCATT TGTGTGTTTGT TTTTAAATGG AATTTTGCA
3201 TTGTGTACCA AAGACTGTAA AATTAAGT TT TAGTATATTT GTA ATAAAA
3251 TTATGGAAT TAATATTGG GCCAAAAATC TGAATGTAAT ACITTTGKCA
3301 AAAACTTTT TTAAGTGTG GCGGAAAGAA GGAGGATG ATA TCTACT
3351 CTGACTTTT AGAATATTTC AAAATATCT ATACTATTA TAANTACATA
3401 TAAACATGTA TTAATATAAA AATTAATAA AATATATAA TGA AGAAGG
3451 TAGTCTTAA GAAATATGTT TCTAATAT ATATCTTGG TCTTAAATTT
3501 AATGAGTGA AAGAGATCT ATATATTA CTATATTA GGTATATTA
3551 CTTGAGTAA TAACTCTCT TGAATCT AG TTTCTATC TTTAAATAA
3601 GTGTAATAAC AAGAGCTTAC TCATATGAT ATATATTIG TAAATATTA
3651 ATAAATAAAG TATATAAAGG AGATATATG SCATATATAT AATATATTA
3701 TAAATGATTA CTAATCTCT CATTATATTT TTTATATTT AATATATTA
3751 ATCATAAA TA AAGAGAAAT AATTTTCTTT GTATATGCT GATATATTT
3801 TTGCTAGAT GAAGATAAT AAGAGATAG TAATATATCA AATATATTA
3851 CGAATTTATA TCTATAAAT STATGTGAT GCAATTTATA TATATATTA
3901 ATAAATAGAA AAAAACTCT TCAATTTTCT TGTAAATCT TATATATTT
3951 CCCCCATAC TCAATGCTTT GATTTTCTTT TTCTAAAGG GATATATTT
4001 TTCTATATTT ATATATATC AGATCTCTTT CTATCTCTG CTATATATTT
4051 TTAATATAT TCTATATCT TAAATATAT TTTATATTA TATATATTT
4101 GATATATTT AAAAACTAA TCAATCTCT AATATATTT TATATATTT
4151 CCAATATTT TCAATCTCT CCAATATTA GATATATTT AATATATTT
4201 TTGCTATAT CATTATATG AAAAAAT TTTATATTA AATATATTT
4251 TTGCTATAT TTTATATTT TTAATATTT TATATATTT AATATATTT
4301 AGCTATATTA TAAATATTT TTTATATTT TATATATTT AATATATTT
4351 GTCTATATTA TAAATATTT TTTATATTT TATATATTT AATATATTT
4401 TTCTATATTT TCAATCTCT AGATCTCT CTATCTCTG CTATATATTT
4451 TTAGTATTA TCTATATTT GGTATATTT CCAATATTA TATATATTT
4501 TTTATATTT CCAATCTCT AATCTCTCT TAAATATTT TATATATTT
4551 TGTATATTT TTTATATTT GATATATTT AATATATTT TATATATTT
4601 AATATATTT AATATATTT AAAAACTTT GATATATTT AATATATTT
4651 TCAATATTT AATATATTT TTTATATTT TTTATATTT AATATATTT
4701 GGTATATTT TTTATATTT GTTATATTT TTTATATTT AATATATTT
4751 ATGATATTT TAAATATTT TTTATATTT TTTATATTT AATATATTT
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4851 ATGATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT
4901 AGTATATTT AATATATTT TTTATATTT TTTATATTT AATATATTT
4951 AGGATATTT AATATATTT TTTATATTT TTTATATTT AATATATTT
5001 TCAATATTT AATATATTT TTTATATTT TTTATATTT AATATATTT
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5101 GGTATATTT AATATATTT TTTATATTT TTTATATTT AATATATTT
5151 ATTAATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT
5201 CTCTATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT
5251 TAGATATTT AATATATTT TTTATATTT TTTATATTT AATATATTT
5301 CTTATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT
5351 GATATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT
5401 GCTATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT
5451 TCTATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT
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6151 TTTATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT
6201 TTTATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT
6251 TTTATATTT TTTATATTT TTTATATTT TTTATATTT AATATATTT

FIGURE 3, page 2 of 24

6301 AAAAATTTCT GTGAAATATA GTTTTGTGA TTTTGATAGG BATTGCATTA
6351 AATCTATAGA TTGCTTTGGG TAATGGAAT ATTTTAACTA TATTTATTCT
6401 TCGAATTGAA AAAATATCAA TATCTTTTCA TTTTGTATG TCTTTTTCGA
6411 TTTCTTTGAT CAACTTTTGA TATTTTTCAG GTAGAAATCT TTAGTATTTT
6511 TTGTTAAATTA GTATCTACTT TATTTCAITG GTAGCTATTG CAAATGGAAT
6551 TATTTTCTTG ATTTCTTTT ACATCTTTCA CTGTTGGCAT ATAGAAATGT
6601 CACTGATTTT TGTAGTTTGA TTTGTAACCT TCGAATTTTA CTAAATTTAT
6651 CAACTTTTAA AGTTCTTATC CGATCTTTTA GCTTTTTCOA AATATAAGAT
6701 CATATCATCT GCAAAACAAAG TAAATGACCT TCCCTCTTTC CAATTTGCAA
6751 GCTTTTTTAT TTCTTTATTT TCTCTGATTG CTCTTCTAG GAATTTCAAT
6801 AATATTTTGA ATAAATTTTG TGAAGTCTGG CATCTTCTT ATTTTCTTAA
6851 TCTTGAAGAA CAGGATTTTA GTTTTCTTCC ATTTGATATA ATACTAGTAA
6901 TGGTTTCTTG ATATATGCTT TTTATTTTGT TGAATTTATG TCTCTCTATA
6951 CTCTATGTTT TGAATTTTCT TTTTATATAA GGGATCTTTA ATATTATTA
7001 AATCTTTTTC AGCAATTAAT AATATGATTA TGAATTTTCT GTTCTTCAAT
7051 CTGTTGATAT GATCTATTTT ATTAATTTAT GTGCTATGCT TGAATCAITC
7101 TTGCTATCAAT GGAATAAATG GCAATTTCTC ATATATAATG ATTTTCTTCT
7151 TGTCTTTTCT TTTCTCTTCT AAGTACAGGG GTATATTTGC AATTTTCTTA
7201 TATAGTTAAA CTTCTTCTAT GCTCTTTTCT TGTACAAATG ATTTCTATCA
7251 CCAATTTATTA AGCTTATTA CCAATTAATTA TTTTCTTCT TCGATCTATG
7301 TATTTCTATG TTTTCTCTCT CATTCTTAA TGAATATCTG TCTTATTTGG
7351 TTTTCTGTTG CTCTATTAAT TTTCTAGGGA TAACTCTTCT TATTTCTGTT
7401 CATTTTCTTA TAAATCAAT GATCTCTATG TTTTCTTAAA AATGATCTTT
7451 ATTTTATTTT AGTTATTA AATATAAAT ATCTATAGT GAAATATAAA
7501 TCAATATAAA TCAATCTATG TATCTCTAT TTTTCTATTT ATTTCTATAG
7551 CTCTCTATCT TTTATTTCT CATAATATA GATTAATATA TTTCTATAAA
7601 AGAATTTTAT TCAATCTATG AATCTCTAT AATTTAATTT CTTTCTTCTG
7651 CATCTCTTTT AATATTTTCT TTTGCAATCT ATTTCTATTT CAAATATAT
7701 TATGAATTTA TTTCTATAG ATTAATATA TTATCTGATG GTATGCTGCT
7751 CTCTCTTTCT TATGATTAAT ATTTTCTAAA ATTAAGGCTT TCTTATGCTG
7801 AATAGTTTGA AGATCTATAT CCAATTTTAA GAAATATAAT AGAGATCTCT
7851 TCTCTGCTCT TTTCTAAATG TCTTTTAAAT ATATCTCTTT GAAATCTAT
7901 AATATGTTAA GAAATCTAGG AATTTATTTA CATTGATCTA GTCAGATATA
7951 GAAATTTTCT AATCTATATG AATCTCTCT TCTCTCTTTA AAGCTCTATG
8001 TCTCTCTCTG TCTCTCTCTG CTTCTAAAT TATCTCTCTT TCTCTCTCTG
8051 TATTTTCTAT ATTTCTAAAT TCTCTCTCT AATCTCTCTA AATCTCTCTG
8101 AATTTTCTCT ATTTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8151 TCTCTCTCTG TCTCTCTCTG TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8201 GTATCTCTCT ATCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8251 TTTGAGGAGA TTTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8301 GTATATAATG TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8351 CTCTAGATAA TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8401 TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8451 ATTTCTCTCT AATCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8501 TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8551 TTTCTCTCTA AATCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
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8651 TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8701 GCAATATAAG ATCTCTCTA TCTCTCTCT AATCTCTCTA AATCTCTCTG
8751 TCTCTCTCTA AATCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8801 AATCTCTCT AATCTCTCTA TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8851 TCTCTCTCT AATCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8901 TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
8951 TCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
9001 ATCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
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9151 ATCTCTCTCT AATCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
9201 ATCTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
9251 GTATCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
9301 TTTTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
9351 ACTCTCTCT TCTCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG
9401 CTCTCTCTCT AATCTCTCT TCTCTCTCT TCTCTCTCTA AATCTCTCTG

FIGURE 3, page 3 of 24

15751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNTAT AAGGTGAGAG
15801 AAGAGGATCC AGTTCGATTC TTCTACATGT GGTTCGCCAA TTATCCCGAC
15851 ATTATCTTGT GAAAGGGTGT TCTTTCCCGC AATTTATGTT TTGTTTGGCT
15901 TTCTGAAGA TCAATTGGCT ATAAGTATTT GGTATATTTT CTGGGTTCTG
15951 TATTCATTCG GATTCGTCTA TTGTCCCAT TTTATAACA TACCATGCTG
16001 TTCTGGAGAT TATAGCCTTA TAGCTAGCTT TGAAGTGGG TAATGAGAG
16051 CTTTCAATTT TCTTTCTTTT GCTTATCTTT TCTTTCTTA TGTGGCTTTT
16101 TTTCTTTCTA TATCAATTTT AGAATTGTTT TT TAATTC GTGAAGATTT
16151 AATGTTTAT TTTCTGCGA ATTCAATTGA ATTGAGATTT TCTTTCTG
16201 AATATCTTCA TTTTCAAAAT ATTGATTTTA CCAATTTATG ACCATGTAAT
16251 GATTTCTTAT TTTCTTTCTT CATTTATCAT TTCTTTATG ATTGTTTCTT
16301 AATTTCTTTT GATAGGCTCT TTCTCTTATA TCTTTATGTA TATCTTTATG
16351 TTCTTTATTT TATTTTATTT TTTCAAACTA TCTTTAAAGG GATTTATTTT
16401 TTATTTTATTT CTCTGTTCTG TCAATTTCTG TATATAAGAG AATCTATTTT
16451 TTCTGTATAT TAATTTTCTA TCTGAAAT TTCTGAAAT TATTTATCTG
16501 TTCTAGAGCT TTTTCTGATG AGTCTTATGA GTTTCTAGG TATACAAACA
16551 TATCATGAGG AATAGAGAACT AGTCTTATTT CTTCTTTTAC AATTTGATG
16601 CTTCTTATTT TTTTCTCTTT TTTCTTCTT CTCTCTGGA CTTCTATCTG
16651 TATCTGAAAT ATAACTGCTA AAATGAGCTA TATTTCTCTT GTTCTATTTT
16701 TATGAGGAA TCTTTCTCTT TTTCTCTCTT TATCTATAAC GTTCTGATG
16751 GCTTTCTCTT AATGAGCTCT TATCTCTTA AATCTATTTT CTTCTATCTG
16801 AATTTCTGAG AATCTTTTAA TCTATAAGAG AATCTTATTT TTTCTGATG
16851 CTTCTTATCT ATCTATCTAG ATCTCTATTT GATTTTCTTT TTTCTATTT
16901 TATCTCTCTT GATCTATCTT TTTCTATTT CAGATTTTAA AATCTCTCTG
16951 CTTCTCTCTT ATCTATCTA CTTCTATCTT GCTCTATCTT TTTCTATTT
17001 GCTCTCTCTT TATCTATCTT AATCTTTT TTTCTATCTT CTTCTATTT
17051 TTTCTATCTA ATCTCTCTT GATCTTTT TTTCTATCTT CTTCTATTT
17101 TTTCTATTT AATCTCTATC TCTCTCTCTG CAGATTTTAA CAGATTTT
17151 CTTCTTTTAT CAGTCTATTA GTCTCTATG GATCTCTATC AATCTCTCTT
17201 TCTCTCTCTG ATCTATCTA CTTCTATTT TTTCTATCTT CTTCTATTT
17251 TTTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT CTTCTATTT
17301 AATCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT CTTCTATTT
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19851 TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT CTTCTATTT
19901 TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT CTTCTATTT
19951 TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT CTTCTATTT
20001 TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT TCTCTCTCTT CTTCTATTT

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14301 ATTTCGATGG AATATCTTTT TCTTTTACCT TAAGTTTACC TGAGTCCTTA
14351 TCTGTTAGGT GAGTCCTG AGACAGACAG AAAGCTGTTT GGTAAATTCT
14401 TATGCAATTCT A AATG AATT CTATAT TTT TAAGT AGGGC ATTAGGGCCA
14451 TTTACATTCG AAGTTA GAC TACAT CGA GGTACATTC TATATCAT
14501 GGTATTTTCT GCTCAATA CTCTGTTT TTTTCATTTG GTTATCTTA
14551 TACA AACT GGSAGATTT TCTTTAAGT AATTG CATT TTGAGTAT
14601 TCAA GATTT GTTCAAAAT TTACAGCTCT TTTTAAAGT TCTCTATIS
14651 CTAATTTGCT AATGCGAAT TCTCAATA TTTGTTGTC TGTAAAGAGC
14701 TCAATTTT CTTCATTAAT GAAGCTTACT TTTAATCAT ACAAATTTCT
14751 TCTTGAIAAA TTGTTTCTTT TAAGGATCT AGAATAAATA CCAATTTCT
14801 TTTTACCTTG TAGGTTTCT GCTCAAAAC CTCTCTTAC TCTATAGCT
14851 TTTCTTAT AGCTATCT AGCTTTTCT CTCTATGCT TTAAGATAT
14901 TTTTCTTCT TGAATTTAG ATAACTGAT GACTATGCT CTAAGCAAT
14951 ATCTTTTCT GATAAATTT CTAGCTCTCT TCTAGCTTA TTTTATTCT
15001 ATGCTAGAT ATCTAAAGGC TGAAGAGCT TCTCTGATT AITCTTAA
15051 ATATCTTCT CAGACTTTA GATTCTCTCT CTCTCTCTCT AACATCAAT
15101 AGTCTTACT TTGGGCTTCT AACTAGCTCT CAGCTTTTTT GGAATTTCT
15151 TTTATTTCT TCTTTTCTA ATTATTTCT TCTTTCTCT TGAAGTCT
15201 AGTAAATTCT AAAGCTTAT CTCTCAAGCT TGAAGTTCT TCTCTCTCT
15251 GCTGATTT ATCTGCTGAG CTCTCTCTCT CATTTGCT TCTATACT
15301 GCTCTCTAA CTCTCAAGAG TTTCTCTCT TTTTATTTA TCTATCTAT
15351 TTTATGAGG AITTTCTCT TTTATATCT GAGATTTCT CTCTTATAT
15401 GCTCTCTAT CTCTCTGAT TTTTAACTT GAGCTCTCT TTTCTCTAT
15451 GCTCTCTTA TTTCTCTAAT AATTTAATT CTCTAATTT TTTCTCTAA
15501 TTTCTCTAT CTCTCTCTT TTTCTCTAT TTTCTCTAT TTTCTCTAT
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20051 AAATAAATA TCATTAAAT GGCATAATG CCCAAAG CAA TGTATAGATT
 21101 CAATG TATC GGTATTAAC TACCAATAC ATTCTT A A GAACCAAAA
 22101 AATATATTT AAAATCATA TCGAATGAA AAAAAGAG C AAATAGTAA
 23101 AGCAATCTA AGCAAAAGAA ACAAAGTAA AGCAAT A C TTACCTGACT
 24101 CAAAA TATA CTAGCAAGT ATCTTAAGA AAAAGCAAG GATCTGGAG
 25101 AAAAAAGAG ACATAAACA ATCGAAGAA ATAAGAG C CAAAAAAG
 26101 GGCATAGAG TA AAATTC TGAATCTTAA CAACTGAG AAAAAAGAG
 27101 ATTGAGAA AGAGCTTCA TGAATTAAT GGTCTGAA TAAATTGCTA
 28101 GGCATAGAG GAGCTTAA AATGAAAT TTTCTAGAG CATATAGAA
 29101 AATAAATTA AGATCTTGA AATATTGAAA TGTAAAT C AAAAAAGAG
 30101 AAAATCTGA AAAAAAGAG GATTAATAA TTTCTAGAG AGCAAGAG
 31101 AAAAAATTA TGAATTAAT AAAAAAGAG AAAAAAGAG AAAAAAGAG
 32101 TGAATTAAT GGTCTTAA AATTAAGAG CAACTAGAG AAAAAAGAG
 33101 CTATTAAT AGCAAAAGAG CAACTAGAG AATTAAT CATTTTAA
 34101 TGTCTTGA TTAATTTG TACTATTTA TTAATTTT TTTTAAAT
 35101 AATTAATTT TTTTCTG TTTTCTG AATTTTCT TTTTCTG
 36101 CTCTTAAT TTTTCTG TTTTCTG AATTTTCT TTTTCTG
 37101 ATCTTGA CATTCTG CATTCTG TTTTCTG TTTTCTG
 38101 CAAATTTT GATTTTGA TTTTCTG CATTCTG TTTTCTG
 39101 TTTTCTG TTTTCTG CATTCTG TTTTCTG TTTTCTG
 40101 ATGATTTT GATTTTGA TTTTCTG CATTCTG TTTTCTG
 41101 CTTTCTG TTTTCTG AATTTTCT TTTTCTG TTTTCTG
 42101 AAAATTTT AATTAATTA AATTTTCT TTTTCTG TTTTCTG
 43101 AGATTTTGA AATTTTCT AATTTTCT TTTTCTG TTTTCTG
 44101 TTTTCTG TTTTCTG AATTTTCT TTTTCTG TTTTCTG
 45101 AGCAATTT TTTTCTG AATTTTCT TTTTCTG TTTTCTG
 46101 TTTTCTG TTTTCTG AATTTTCT TTTTCTG TTTTCTG
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 78101 TTTTCTG TTTTCTG AATTTTCT TTTTCTG TTTTCTG
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 98101 TTTTCTG TTTTCTG AATTTTCT TTTTCTG TTTTCTG
 99101 TTTTCTG TTTTCTG AATTTTCT TTTTCTG TTTTCTG
 100101 TTTTCTG TTTTCTG AATTTTCT TTTTCTG TTTTCTG

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25201 TGGCATGTGA GATGTGCTT TCA TTTCTT CCGTATTGT GAGGCTTCC
25251 GAGGCACTG GAACTGTGAG TCCATTAAC CT TTTTAT TTTTATTTT
25301 TTTGTAATTT GGTCACTCTT ATGATCTCT TTAT TACGAG CATGAAACA
25351 GACTAATACA AATATCTAT AGTAAATTT GC TATAGTT TCTTTTCTG
25401 ATGTGTCTTT GTTTTCTGTA TCAATCTAAT ACCTGCTTTG TAGAATGATA
25451 TTAGAAGTAT TTTCTCTAAT TATAATTTT AGAATCTTT GAGTAGAATT
25501 GGTGTGATTT ATTCTTATTT TTTTATTTT GATACAGGGG CTCAATCATG
25551 TTTCTCAATC TGGAGTCTAG TGGTAAATC TTAGTTCCTT TCAACTTGA
25601 CTCTCCAAAC TCAGGCTATC CTCATCTC AGTCTCTGTA GTAGTCTGTA
25651 CTACAGCAG GTGCTCATTT GCTCTATATA TT TTTTATAT TTTTATAGA
25701 GATAGACTTT TTTTCTTAT TCTATCTAT TCTATCTAT ATCTCTCAA
25751 AATCTGCTTT AGTATCTATT TTTTATCTT TCTATCTAT GTCTCTCTA
25801 TTAGAGTAG TTTACAGAGC AATCTCTAT TATATATAA TTTCTCTTT
25851 TTTCTCTAT TTTATCTCTT CTCTCTATTA CTCTCTCTT ATTCTCTTA
25901 TTTTCTCTT GATTCTCTTA CTCTCTCTT CATCTCTCTT AGCTCTCTT
25951 TCTCTCTCTT AAAAAGCTT CATCTCTCTT TTTCTCTCTT AGCTCTCTT
26001 TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT ATATACTAT CTAGGCTAAA
26051 AGCTCTCTT TTTCTCTCTT TTTCTCTCTT CATCTCTCTT TTTCTCTCTT
26101 TCTCTCTCTT CCACTGAAA GTCTCTCTT AGCTCTCTT AATCTCTCTT
26151 GATCTCTCTT AGCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT
26201 CTCTCTCTT GAGCTCTT CBTCTCTCTT CTCTCTCTT TTTCTCTCTT
26251 GTCTCTCTT CTCTCTCTT TATCTCTCTT TTTCTCTCTT ATATCTCTT
26301 CTCTCTCTT GTCTCTCTT TTTCTCTCTT ATATCTCTT AATCTCTCTT
26351 CTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
26401 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
26451 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
26501 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
26551 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
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26651 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
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28751 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
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29251 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
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29601 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
29651 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
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29851 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
29901 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
29951 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT
30001 TTTCTCTCTT GTCTCTCTT TTTCTCTCTT TTTCTCTCTT TTTCTCTCTT

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44101 TGGAAATAG CAATTGTAA TTCTATGTAC TTTTAAAT AATGTTACAT
44151 AAGA TCAT ATTCTATTT TTATTAAA GGTAGAAAG AGTTCAAGAT
44201 AATGTTTAA ITTGTTACAG TGTTTATA GTTT ATTC TAGACTTCA
44251 CATA TT T AAAATTTAT AGATT AGC CASI TASA AATCTGATG
44301 TCCTGAA TA TAACTTA T ACTTCTTGT AGSA AGAA GACTTAAAA
44351 TATCTTAT ACTTAATGAA TATCTAAAG ACCA CTAG AGATCTCT
44401 AA CTGCAAA CTTA TCTT CTCTAAAG GCCA AAAT GCTATTCTG
44451 AGTACTT T CTAACTCTT CAATATAG GATCACTT GCAACTTTTA
44501 GAATAGTTC TTTATTTT AGATTTTT TATA TTAC TTTTITAA
44551 ACAGTATTA AATTTCAGAT CAGTICATC TGAATTTA AGCTATCCAG
44601 ATATTTT TA TACTTACGA TTTTGATGA TATTGAAGA CTTIAGAAAG
44651 CCTTATTA TTAICTAAAG CTCTGCAAG CTAAATTT ATTTTCAAT
44701 TGAATTTTAA ATTAAATTA TTGAAAGGA AATAAAAT STTGAAAGAG
44751 TTTTAAAT CAGGATGAG TTTTCTCC AAACTATAC ATTTATAGG
44801 AAATCTGTT TTTTCTTCT TCTGACAAA TATTAGATT TAAATTTACT
44851 TTAAGTTCT AGTATTAAAC AGGTTAAAC AGATAAATC CTTAATAATC
44901 TCTTTTAA TAAATTTTA TTTGAAAGCA CATTAAATG TCTTCTAATG
44951 CTCTGATTT CAGTTTAA CTTAGAGAGA TTTTAGCT CATATTTCT
45001 TCATCTTGA AATAAGGAA GTTAAATAC TCTATTTA GCTCTTAA
45051 CTCTGATCA AAAATTAAG TTTGAGGAT TTTTAAATG AGCTGTTGGG
45101 ATCTGATTT TGAATTTAT TGAATTAAT TTTTAAATG STAAATTAAT
45151 TATCAAAAT GCAATTTTA TAAAGTAAAG CACTATTT TTTTITTT
45201 GATAGTAA TTTTCTCTG TTTTCTAGG TGAAGAGCA TCCTATCTC
45251 TCTGTTAA TGAATTTCT CTCTGAGGT TAAATTAAT CTCTGCTC
45301 AGCTCTGAA GTATTTGTA TTAATTAAT GTTCTATAT GCTCTTAA
45351 TCTCTTCT TTAATTAAT CTCTGAGGT TAAATTAAT CTCTGCTC
45401 CTGAACTCT GACTGATCT GACTGATCT CTCTGAGGT TAAATTAAT
45451 GATATTAAG GTGTTAGCT CTCTGAGGT TAAATTAAT CTCTGCTC
45501 CTTTATTA TAAATTAAT TATGATCT TCAAAATTT GTGTTCAAT
45551 AATTAAGCA TATTAAGCA ATTATGCT GATGATTT TATATAGAA
45601 TTTATTAAT TTTGTTGCT TTTGTTGCT TTAATTAAT TCAATTAAT
45651 GTATTTAAAC ATGTAATTA ATTGATTAAT ATCTGATCT TCTTATTA
45701 AGATATAAT TGTTATGCT GATGATCT TCAAAATTT GTGTTCAAT
45751 AAATTAAT GTTATTAAT TATGATCT TCAAAATTT GTGTTCAAT
45801 CATTATTT CACTGATCT GATGATCT TCAAAATTT GTGTTCAAT
45851 TAAAGTAA TTTTCTCTG TATGATCT TCAAAATTT GTGTTCAAT
45901 CTAATTAAT ACTTAAAT TTAATTAAT TCAATTAAT TCAATTAAT
45951 ATATCTTAA ACTTAAAT TTAATTAAT TCAATTAAT TCAATTAAT
46001 TCTATTTGTT ATGATTAAT ACTTAAAT TCAATTAAT TCAATTAAT
46051 ATTATTAAT CTGATTAAT AATTAAT TCAATTAAT TCAATTAAT
46101 ATGATTAAT TCAATTAAT CTGATTAAT TCAATTAAT TCAATTAAT
46151 TCAATTAAT AATTAAT TCAATTAAT TCAATTAAT TCAATTAAT
46201 CTCTCTGCT CTGATTAAT ACTTAAAT TCAATTAAT TCAATTAAT
46251 ATCTATTAAT ATCTATTA TTTTATTA TCAATTAAT TCAATTAAT
46301 ATCTATTAAT GCAATTAAT CTCTGATTA TCAATTAAT TCAATTAAT
46351 AAAATCTG GCAATTAAT CTCTGATTA TCAATTAAT TCAATTAAT
46401 ATGATTAAT AATTAAT TCAATTAAT TCAATTAAT TCAATTAAT
46451 AAAATCTG CACTTAAAT TCAATTAAT TCAATTAAT TCAATTAAT
46501 CACTTAAAT AAAATCTG TCAATTAAT TCAATTAAT TCAATTAAT
46551 CACTTAAAT TCAATTAAT TCAATTAAT TCAATTAAT TCAATTAAT
46601 AATTAAT TCAATTAAT TCAATTAAT TCAATTAAT TCAATTAAT
46651 AATTAAT TCAATTAAT TCAATTAAT TCAATTAAT TCAATTAAT
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47101 TCAATTAAT TCAATTAAT TCAATTAAT TCAATTAAT TCAATTAAT
47151 TCAATTAAT TCAATTAAT TCAATTAAT TCAATTAAT TCAATTAAT
47201 TCAATTAAT TCAATTAAT TCAATTAAT TCAATTAAT TCAATTAAT

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47251 ACTACAAAAA CACAGAAGAC AACCTAGGCA ATGCCATCCT AGACATAGGA
47301 ACACGCGAAG ATTTTCATGAC AAGATATCA AAAGCAATTG CAACAAAGC
47351 AAAAATTGCT AAATGGGATT TAATTAAATG AAATAGCTTC TAAACNAAA
47401 AAGAAATGAT GAACAGAGTA AACAATAAAC CTAAGAATG CAAGAAATAT
47451 TTACAAAAAT ATGCATCTAA AAAAGCTTA AAATCCAGTG TCTATAGCA
47501 GCTAAATATA ATTTACAGAA AAAAAATGCT ATTAAATGCT GGTCAAAAGA
47551 CATTAAATAA TGAATAACA TAATGCTGCT AAGTTAAT ATGAAAAAG
47601 CTATTAAGTG ATCATTTAGG AAATGAAAT CAAATACAA ATGATATAGC
47651 ATCTAATAA AGTCAGGATG GTTAAAGATA AAAAAATGCT GTCAAGAAAT
47701 AGTAATGCT GGCAGGCTG TGAAGAAAG CAAACATTA TACACTATTA
47751 GTGATATCT AAACATGCT AAGATATCT GAAATATCT TAGTGATTCT
47801 TCAAGGAGCT AACAACAGAA CTAATATCT AAAAAATGCT GGTATTAATG
47851 GATATATACT CAGAGGAAAT TAATTCATCT TAAATATCT ACACGCTCAT
47901 GATTAATCT ATTCAGGCT TAATCAAT GATTAATCT TGAATATCT
47951 CTAATGCT ATCAATTA GATTAATCT AAAAAATGCT GTACATATAT
48001 AATATGAAAT AGTATATCT CATAAGAAAT AATATATCT TCTATATCT
48051 AAAAAATGCT ATGAGGCTAG AGGATATCT TCTATATCT CTAACAAAGC
48101 AAAAAATGCT CAAATATCT TCTATATCT TATAAGGCTAG AGTAAATCT
48151 TGAAGATCT TGAATATCT GAAAGGAAAT ATCAATCT GGTATCTCT
48201 GATTAATCT GGTATATCT TGAATATCT GATTAATCT AAAAAATGCT
48251 TATTAATCT TGAATATCT TGAATATCT TGAATATCT AAAAAATGCT
48301 TGAATATCT TGAATATCT TGAATATCT TGAATATCT AAAAAATGCT
48351 ATAAATCT TGAATATCT TGAATATCT TGAATATCT AAAAAATGCT
48401 GGTATCTCT GGTATCTCT TGAATATCT TGAATATCT AAAAAATGCT
48451 GGTATCTCT GGTATCTCT TGAATATCT TGAATATCT AAAAAATGCT
48501 AAAAAATGCT AAAAAATGCT AAAAAATGCT AAAAAATGCT AAAAAATGCT
48551 AAAAAATGCT AAAAAATGCT AAAAAATGCT AAAAAATGCT AAAAAATGCT
48601 TTTCAATCT TTTCAATCT TTTCAATCT TTTCAATCT TTTCAATCT
48651 TTTCAATCT TTTCAATCT TTTCAATCT TTTCAATCT TTTCAATCT
48701 AAAAAATGCT AAAAAATGCT AAAAAATGCT AAAAAATGCT AAAAAATGCT
48751 AAAAAATGCT AAAAAATGCT AAAAAATGCT AAAAAATGCT AAAAAATGCT
48801 TCTAATCT TCTAATCT TCTAATCT TCTAATCT TCTAATCT
48851 CCAATCTCT CCAATCTCT CCAATCTCT CCAATCTCT CCAATCTCT
48901 TACTAATCT TACTAATCT TACTAATCT TACTAATCT TACTAATCT
48951 CATTAGATCT CATTAGATCT CATTAGATCT CATTAGATCT CATTAGATCT
49001 TACTAATCT TACTAATCT TACTAATCT TACTAATCT TACTAATCT
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50251 TACTAATCT TACTAATCT TACTAATCT TACTAATCT TACTAATCT
50301 TACTAATCT TACTAATCT TACTAATCT TACTAATCT TACTAATCT
50351 TACTAATCT TACTAATCT TACTAATCT TACTAATCT TACTAATCT

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50491 TGGTTCCAGG AATTGATTA AATCTCTGTA AATCAATAA CTGAATAAG
50492 CTAATGGAGG AATATTTTCA GAGGCGACAG ATACCAAAAA AATATAGGTT
50493 TTACAAAATT AGTTAA AAA ATTAAGCTAAA CCACCAAGAA CCACAAIAAG
50494 GAGGAAAGG AAGATTAAGG SACTGGGAGA ATTAATCAA TTTCAGAGAT
50495 TTTATATTA TAAATTTAA AACATCTGTT TTCTAAGAAA AAAAAAAA
50496 TTAGGATTT GAGAAAATA GAAAATATGG CAAAGA AAAAAGCAAAA
50497 CCGCAATTC TCAATATAG GTGAAATGG AAATATAGA ATATTCGAG
50498 AAGGATCGA ACATATAGCA CCGATCTGTT TCAATAGGG GAGATGATA
50499 GATTATAG ATATATTA TGGATCAGG AATATATAT GATATTTTA
50500 TATATATG ACAAATTTGG ATGTTTATA CATATAATT AATTTTAAA
50501 GTATAATAAA AATGAAATG AAAAAAATC ATTTAAIAA AATATAA
50502 TATAATTT ATATATTTA GCAATATTC TAAATATAA AATATTA
50503 TAAATTAACA AATATTAACA GAAAAATCA CATATGATAT TATAATCAT
50504 ATGGAATAC TGAATTTT CCATTAAGA TCAATAGCA GATATGATG
50505 TTATTTTGG TTGAAAAAAA TAAATATAT AATTTTAAAT TTCTTAAGTG
50506 GTATGAATTT GTTTTGTGGC CTAAATATAG ATATATCTG GATATATTT
50507 TTTATTTACT GAAAAATAAT GTTATATCTG CTAAATTTGC CAAAAATCTG
50508 GATTTAAGA AGTATCTTA GTTCTGATG GAGCTGAGG CTTGAGGTTG
50509 TGTGATCTAG CTTTCTTGG AGTCTGTTGG AGCTGATCT GTGATTAAG
50510 CTTGATCTG AATGAGGAG CCGAATATCT GAGGAGCA GATATGATCT
50511 GATATCTGTA CTTATAGGG GTTATATAGA GTTGAATTT TTGATATCTG
50512 AATGATCTG TTTGATATG GATGATCTG TGAATCTAG GTTATGATCT
50513 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50514 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50515 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50516 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50517 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50518 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50519 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50520 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50521 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50522 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50523 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50524 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50525 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50526 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50527 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50528 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50529 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50530 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50531 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50532 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50533 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50534 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50535 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50536 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50537 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50538 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50539 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50540 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
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50543 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50544 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50545 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50546 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50547 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50548 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50549 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG
50550 GTATGATCTG CTTGATCTG GATGATCTG GATGATCTG GATGATCTG

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52551 ATTATATTGG CTACTTTTTT CCCATTTTCT CCATCCATTT TATCCACCA
52552 TTTGTTTTAT AACTGTGAAT ATTTGAAACC ATATTTTTCT TTTCTTTTT
52553 CTTTCTTTCA GACTGASPTT CACTTGTGCG CCAGGCTGA A GTCCAATGGC
52554 GGAATTCGA CTCACTGAAA CTTCACTTC CAGCTTCAAA GWAATTCTCC
52555 TGGGTCAGT TCCCAASTAG CTC AACTAG AGGCGCCCT CACACCGCC
52556 AGCTAATGTT TGTATTITIA GTAGACAA GCTTTCAG TA TCTTGGCCAG
52557 GCTGTCGTA AANTCTGAC CTCGCTGAT CCACCCAC T CAGCTCCCA
52558 AAGTCTGCT ATTAACAGGTA TGAACACTG CCCTGCGC A AAACATATIT
52559 TTTCTACIA TCTCTCTTC AAATTAATG TACTGACAT ATATCTTCIG
52560 ACAAATAGC TTTTAAAGC AAGTATGAA AACAACATTT GAAATATTTT
52561 TTCTACATAT AANTGAGCTT TGCATTCAG A AAAGAT A CTGTGAA
52562 CTTTAGAAA CAAATCTTTC TGAATTTGGA AAAAATAIGA AATCTATCTG
52563 AGAGACTTCT AAGCTCTTTT AGTTCTAGC A AATCTTCT AGAATTTCCA
52564 TTTTAGIAT AATTAAGCT AGGCTATTTG GCTCTGCTA TTTATGTCG
52565 AATATAGT TAACTATCT TTTTITTA GATACTCA CTTGAGTCCG
52566 AAGTACAAG AATCTTTTGA TGTGCTCTT AACTCTTTG CAAAGTTTTT
52567 TGCATACAT AAATAATAC AAAAGGAGCG AATAAGAT AAATACCTT
52568 TTTCTAAAT CTCTATTTT CTCTCACTCT TATTTTTT ACTGAGCAAA
52569 AATAAATTT TCTTAATAT ATAGTATCT TTTGAGCTG GCTTAGTCTT
52570 CTTCTATTC TCTATCTCT CCTCTGAAAT TCTCTGCTT GAGTTCTAT
52571 TAACTTAA AATCAAGAT CAATATAGCT AITATCAAC ATAGCTCAAT
52572 TAGAATATG ATATACTAGG TGTGAATTA CTTGAGTAT GTGACCTTT
52573 AAGCTTCTT AACTCTCTTC AACTTAAAT TCTATTAAG ATCTTAAAT
52574 AATCTATTA TCTCTGAT CA AAGAACT GCTTTTTT TTTTATTTT
52575 TAACTCTT GATCACTCT CTTCTCTT TCTATCTT TCTATCTT
52576 CTTCTATG AAAATCTAA AAGATTAAT CTTCTATCT CACTTTACTT
52577 TCTCTATTA GCGAGTACT GAGCATCTA AATATTTAA TAGATATGA
52578 AAGCTAGTG TANGATAT GTATAGATAG AATCTCTAA ATGCTGCGAA
52579 AATCATTTA GAATCTATTT AGTCAAAAGA CAATACATTT ACAAATAAT
52580 CTATCTCTT ATCTCTCTAG ATTTTCAAAA ATCTCTCTT ACAAATAAT
52581 AAGCTCTTA GAGTACTTA AATATCTAC TCTCTCTTA AATCTCTTA
52582 GAGCTCTTG AGCAAGCTCT AATCTCTTA AATCTCTTA AATCTCTTA
52583 CCACTTAA CTTCTCTAT TATATAGCTA GCTCTCTTG CTTCTCTTG
52584 AATTAAGT TATATAGCTA GCTCTCTTG CTTCTCTTG CTTCTCTTG
52585 CCACTTAA CTTCTCTAT TATATAGCTA GCTCTCTTG CTTCTCTTG
52586 TTTCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG CTTCTCTTG
52587 TAGAAGTAA AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52588 CTTCTCTTG CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG
52589 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52590 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52591 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52592 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52593 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52594 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52595 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52596 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52597 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52598 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52599 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52600 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52601 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52602 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52603 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52604 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52605 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52606 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52607 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52608 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52609 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52610 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52611 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52612 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52613 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52614 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52615 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52616 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52617 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52618 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52619 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52620 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52621 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52622 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52623 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52624 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52625 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52626 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52627 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52628 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52629 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52630 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52631 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52632 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52633 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52634 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52635 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52636 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52637 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52638 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52639 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52640 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52641 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52642 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52643 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52644 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52645 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52646 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52647 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52648 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52649 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52650 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG
52651 CTTCTCTTG AATCTCTTA TATATAGCTA GCTCTCTTG CTTCTCTTG

FIGURE 3, page 18 of 24

56751 GAATTTTTTGG CCGTTTGCTT GAATTCCTGG AATGCATACA TATAAGCTAA
56751 AGGATATGTTT GCAGTTATAA ATGTCATAAG TACAGGTACA ATCTCAGCCT
56751 GTTCTTTAGA AACATTTCOA TACAAATCGC TAAATAAATT TCACATTITIT
56751 GTTAGTTTAA TATATACATG AGTTTATTTG TGATATAAAT AATAAATACA
56751 GAGAGTGAGC ATATCACAGA GGAAATTTCT TAAAGATGA TTTTAAAAAT
56751 CAGCTCTAGC AAGAGCTTAA GATTAATTGG TCATAGAACG GCATTTGACG
57001 CTTAAATTA TGACCACTTC ATCTCTGAG AGGAGATCT AGCTTTGCTG
57001 ACCGATTTAT ATTACTTTTA AATTAAGAA CACTCATTTA ATAAAAATA
57001 ATTTTAAAAA AAATATTAAG AAATAAAAT : AACTGAATCT TTTATTATA
57001 GAAATTAATA GAAATAATAA AAAGTTTCT GAGTAAAGG TTTCTCTCTT
57001 GTCCATATAA GATAAGTTA AGAGTTCTT AGATAATTAT AAAACTTTCT
57001 AAAAAAGTAA AAATGTTACA TTACTATACG TACTCAGATT CACTGCTTAA
57001 AGTATCTTAA AATCATTTCA ATCTGGAAG AAAAGCTGAA CTTAATCTCT
57001 GCTCCTTAAA AAGGGAAGCA CAAACATAAG TCTAGCTTCA AAAAAGGAAA
57001 ATATTTTAGG CTTTGGTGGG AGGCTGGAGT TTATATAAAA TTTAAATGAA
57001 GTAGGCTTTT AATACTTTCA AAGAAAAATA AGCAATGAG CAAACTTAAA
57001 GTACTGCTCT TGAAAAACAT AGAGTCAAGA TAAATGTATA CTSTATGCTT
57001 AGTGGGAGCA GAAATGCAAT CATCTTGATA AATTTTGAGA TACATCTGCT
57001 CACTCAGTAA TTTCAGAATA CATCAATGC ACTAGCAAGT TAAATTTGAT
57001 AGAATACATT TGAATGTTA AATGAATTA GCTAGGCAAA GAAAGACAAA
57001 CACCAATGAA TTTTACTCAT ATGTGGAATT TTAAGAAAT GATCTCAGCT
57001 ATATCTGAAA TTTTAAAAAG TTGATCTCAC ACTAGTAGAG GGTAGAACTG
57001 TTTTATTAAG GGGCTAGGGA GAGAAAGGAG GTAGAGGCA TGAAGATGCT
57001 TGGTCAATCT GTATAAAGTT AGAGCTAGGA AGAATAAAT TTTGTTATTA
57001 CACAGTAGAG CTGACTATAG CAAATATTA TCTAGATGT ATTCTAAAT
57001 ACTAGAAAAA GAGGCTTTTT AAAGGTCAGT ACAAAGAAAT AACAAATTT
57001 TATAGTCTG GATATGTTAA TTAGCTTAT TTGATCTTAA TACTGCTGCT
57001 ACATGCTCTG AAACACCAAA TTGATCTTAA TATATATGTA CAATTATGCT
57001 CCAATTATAC ATTTAAAAAA TAAATTTTAA AAACCTTCAA TTAACCTCTG
57001 GTTTAAAAAA AAAATATAAA CCAAACTTAC ATGATCTCTA AAACAAATAA
57001 TATCATGTA AACTCTTCAT ATCAGAACTC ATGAGTATAA TATAAGCTAG
57001 TGATCAGAG AAATTTTATA ACTAAGTACT CCAATTTATA AAAATTAAG
57001 ATGAAAAAAT AATTGATTAA ATATTGAACT AAATAAAAT TTTAAATGCT
57001 GTAGAAATAT GTGATATAC TTGACTCTTC TCACTCTCT GCTTCAAAAT
57001 AGTTAAGGAG ATGACTTTTA AGTATCTCT TTTTAAAGCA AATTAAAAAA
57001 AAATTTTCAA ATGCTCTTTG GTAGAGTCT AGTAAATAC ATTAAGGAGC
57001 TTAGATTAG TAAACAAAT TAAATTAAG AAACAGAG ATTAAATAAA
57001 AAAGTAAATA TTAACAAAAA GAATAGAAAT AGCTAGAGC TAGTAAAGCA
57001 ATCAAAAGCT TTTATTTTAA AAAAGATTGA TAATCTAGAG CAAACCAATTA
57001 GCTAATTTAA TTGAAATAAA ACTAGAGGAG CAAAGTATG CAAATTAAG
57001 AACTGGAATA TAACATTTAG AAGAAATTTA AGCAATGTA AGAGATATCT
57001 TTGAGAGCT CTGTCGAAC AAATTTTAAA ATCTAGATGA TAGAGATAT
57001 TTCTAGTAA AGTAAAGATT AGTAAAAA ATTTTATTAG AGATATGAAA
57001 ATTGAAGAGC TCAATCTTCA TAAAGGAAAG AGTAAATAT TTTTAAAAAG
57001 AAGAAATATA GAAATTTATA AAGAACTACT TAAATAAAG TATCAATCTC
57001 CAGATAGTTT CACAGGAAA TGCTATGAAA CTTTAAAAAA CCAATATAGC
57001 TCAAGTAACT TCTGCAAAAC AGTCTTTCTT CTGAAAAA TAAACAAAA
57001 TATAAGAAAA CTATACATAA ATATTGTAAT CTAATTTGCA AAGTTGTTCT
57001 TAAAGGAGAT ATCTGTAGAC AATCTTAAA CAGCTATAA TGTATATTA
57001 GATTAAAAA ATAAGTAAAT GAAGTATAG TGAGAGTAC AAATTAATCA
57001 GAAGCTAGAG ATGAACTATG TGCTACTGGA TCTGATTCAG AGCATGCTG
57001 ATCTAATCAA GTTAACTTAA ATATTGATAG AGCTTAATAG ATACAAAAAT
57001 AATTAACTAT GCTATATAC ATGATCAAT ATACATATCT ATAGTTCTTA
57001 CCGCTGCTCT CTAGAGGGC CTAGAGGAAA TAGTACCTTA TAGCAACAA
57001 GCACAGCTAA TGCTAAGACC TTGATCTCTA AATATCTCT CCAATA (SEQ ID NO:3)

FEATURES:

Start: 104
Exon: 104-104
Intron: 104-10478
Exon: 10479-10488
Intron: 10489-10513
Exon: 10514-10539

Intron: 54740-54281
 Exon: 54282-54388
 Intron: 54389-55020
 Exon: 55021-55202
 Intron: 55203-56284
 Exon: 56287-56445
 Stop: 56446

CHROMOSOME MAP POSITION:
 Chromosome X

ALLELIC VARIANTS (SNPs):

DNA			
Position	Major	Minor	Domain
7107	T	C	Intron
7108	A	T	Intron
8661	C	A	Intron
12620	T	-	Intron
27414	G	A	Intron
41717	T	A	Intron
41718	T	G	Intron
41719	A	G	Intron
46148	T	A	Intron
48183	C	T	Intron
48217	C	T	Intron
48470	A	G	Intron
49542	T	C	Intron
49826	G	C	Intron
52861	T	G	Intron
51703	T	C A	Intron
55624	G	C	Intron
56467	C	A	Beyond ORF (3')
57395	C	T	Beyond ORF (3')

Context:

DNA

Position	
7107	TTGAATAACCTGTGGTGAAAGTGGGCATCCTTGTTATGTTCCCAATCTTAGAGGACAGGAT TTCAGTTTTTGTCCATTTCAGTATAAATACCTAGCTATGGGTTTGTTCATATATGGCTTTTATT CTGTTGAGGATATGTTCCCTCTATACCCATGTTTTTGAGGGTTTTTGTTCATAAAGGGATG TTTAATATTATCAAATGCTTTTTCAGCAACAATTAAATGATCATGAGGTTTTTGTTCAT CATTCCTGTTGATATGATGTATCTCATTAAATTGATGTGTATGTTGAATCATTCTTGCAT [T,C] ACTGGAATAAATTGCACCTTGGTATGATAAATGATCTTTTGTGTTTGTGTTTTTGTCTTCACT TTTAAGTACAAGGGTACATGTGAGATTGTTATATAGGTAAACTTGTGTTCATGGGTGTT TGTTGTACAAATTATTTTCATCACCCAGGTATTAAGCCTAGTACCCATTAGCTATTTTTTT TTCAGAGTCCATGATTTCTCATCTTTTAGCTGCCACTTGTAATGAGAAATGTGTGGTATT TGGTTTTCTGTTGCTGCATTAATTGCTAGGATAATGGCTTCTAGCTCTTTCATGTTT
7202	GGGTTTGTTCATATATGCTTTTATTTCTGTTGAGGTATGTTCCCTCTATACCCATGTTTTT GAGGGTTTTTGTTCATAAAGGATGTTTAAATATTATCAAATGCTTTTTCACCAACAATTA AATGATCATGAGGTTTTTGTCTTCATTCTGTTGATATGATGTATCTCATTAAATTGATG TGTGTATGTTGAATCATTCTTGCATCACTGCAATAAATTGCACCTTGGTCAATGATAAATGA TCTTTTGTGTTGTTTTGTTTTCACTTTTAAGTACAGGGGTACATGTGCAGATTTGTTAT [A,T] TAGGTAAACCTGTTCATGGGTCTTTGTTGACAAATTATTTTCATCACCCAGGTATTAAG CCTAGTACCATTAGCTATTTTTTTTCTGAGTCCATGTATTCTCATCTTTTAGCTGCCA CTTGTAAGTGCAGAAATGTGTGGTATTTGTTTTCTGTTGCTGCATTAATTTGCTAGGCATA ATGGCTTCTAGCTCTGTTGATGTTCCATATAAAGGACATGATCTCATTCTTTTTAAAAA GTGACTTTATTTTATTTTAGTTACATAAATTACAAAATATCACTAAGTGAAAAATAAATC

FIGURE 3, page 20 of 24

TGGCAAGGAGTCTAGTTG : TTGGTGGCGTAGAGCTGCATGTTTAGATTTTGCAACAAT
TGGCAAASTGCTTTCCAGT TTGGTCATACIATTTACAIATAAACCAAGCACTATTTCGTG
GATTCCTACAGCAATTTT TGTCTCAGIATTATTATCTTAACATATTTGAAAGGTG
TAGTGACATTTTATTGTTTAAATTTCATTTCC AAAAAGCAATAAAATTGAACATTT
GCTGCTTATTTTGTCATCTTATCTCTCTCAATGCAATGCTGTCATGTTTTCCT
[C,A]
ATGCTCTTTTTCCTTTTTTATTCTAGAGATTAGATTTCGCAATAAAGATTGATATAT
TCAATGTATACAACAATATTCTTTCTTTTAAAGAAATTATTATTCTCAAG
GCTTTTGGGGAACAGGTGAAGTTTCTTACATGATTAAGATATATAGTAGTATTTCAG
AGATATTGGTGCATGGTCAACCAAGCAGIOTACTGTACCAATGTCTAGTCTTTAT
CTCACTGCGGCAAGCTTCTCTCAATCTCAAGTGCATTGTATCACTCTATGCTT

[illegible]

CTTACTGCGAAGCGCTCTTCTCTCTGAGTTTTCAGAGCAATTTCTCTGCGGCGAGTTCTCTCAAGTAG
CTGGGATACAGGAGTTCAGCACTATGCGGCACTCAATTTTATAGTAGAGATGGGATTTTCAT
CATGTTGCTCTAGGCTCTCTCTCGAAAGCGCTGAGTTTCAAGTCTATCTGCTCTGCTTAGCGCTTC
CAAAAGTCTTAGGATTACAGGCGATGAGGCCACCAACTTTGGCGCTTCTCTGCGCATTTTAAAA
CTTGGGTAGTTAAGTTCTTAGATTCTCTCTTTATTTGTATTTTATATGTTATAGATACA
[E.A]

GAGTTTTTTATTCTTTAATAAATTTTTTGGAAAAGCAGGAGATTTTATTTTCTCTTAAG
CTAGCTTATGGAATTTTTCTCTCTCTCTCTCTCTCTGGAATTCAGTCAATGACCTCT
TTAGTCTTTTATAGAGATGATGCTTAAGCTTATTGGAAGAGCTTTGCACATCTTATTCG
CTTTTAAAGATGCGCTCTCTCTGAGATTATCTAATTAAGCTTTACTTATCTTTTAAAG
TAACTTTAATCTACTTCTTCAATAGAAAGGCTTTCTGAGACAGAGCGGATATAGAGCTCT

AAATCCAGCTTTCAATAAGGAAGAGTGAATCATTTCCATGTTGATATAAAATAGCGAA
 AAAATTGTATTTTTCGAAAAATAGCACTTTGTGCACCTCTATGCACTTTTAAATTAAGGTT
 ACATAAGAGTCATGATTTCTATTTTTGACTTAAAGGTACAAAAGAGTTTAACATAATGTT
 TAA'TTTTGTACATGTTTATATAGTGTGATTTCTACACTTTTCACATAGTTGTTAAATTT
 TTATACAATTGAGCGAGTTTCTACAAAAGTCTGATGTTTCGAAGGATAAATTTTACTTTG
 (T,A)
 TGTAGGCACAGAAAGAGCTTAAATATTTCTATTAATTAATGAATATGTTAAAGACCAAGC
 TAGAGTATTTTCTAAGCTGAAAACTTAGTGTCCTCTGGAAAAAGGCCAGAAAGTTGCTTACT
 CTGAGTATGTTGTCTAACTTTGTGAGATATAGGATCATCTCTGCAACTTTTAGAAATAG
 TCTGTTTATATCTGCAGTAGTCTTTTATATTGCACTTTTAAAAAGCAATTAAGATTGGA
 CATCAGGTTACTCTGAAATTTTAAAGGATACAGATATTTTCTATAGTCCAGCAATTTCTGA

GAATTCGATTTTGAATTAAGGTGAGGAAAAAGATTGAACATAAATCTTTAAATTTTGTCATA
CTGCTTTTATATATTTTGATTCTAGCTCTTCATATATTGTTAAAAATTTTATACAAATTCAG
CTAGCTTGTAGAAAAGGTGTGATGTCTTGAAGAGGAAAAATTACTAATTTTGTGTAAGGATAGAA
AGACCTTAAAAATATTCTTATCAATTAATTAATATGTGTTAAAGATCAGGCTAGAGTATTTTC
TAAGCTGGAAAATTATTTAGCTTGAAGAAAAGGAAAGAAATTCCTATTCTGATAGCTCT
{T,G}

CTAACTTTCTCAGAAATATAGGATATCTCTTAACTTTTAAAGAAATAGTGCCTTATATTGC
AGCAGTCTTTTATATATCTTCTTTTAAAGAGGATTAAGAAATTCGAAATCAGCTGATCT
TGAAGCTTTAAAGGGGATAGGATATTTCTATACCTGGAGGATTTTGATGACATTGAAGA
CTTTAAACAGGCTTATGAATTAATTAAGGCTCTGTGAAGGAGAAACATTTATGTTAAAT
TGAATTTTAAATTAATATATTTAAAGGAAATAAAAAATCTTGAAGAGATTTTAAAAAT

ACTCTGAAACCTTAAAGCTACCGATATTTTCTATACTGCAAGATTTCGATGACATTGA
AAGACTTTAAACAGCCTTAGTAAATTATTAAGGCTCTGTAAAGCAACATTTATGTTG

49826

52861

54703

55624

56467

FIGURE 3, page 23 of 24

CTATTAAGGATAAATAATCTGTCCACTGTATTTACAGGTCTTCATACTTTTACTTAATT
TTCTTTATCTGTATGGGAAACCACTGCAATCCTGAATGACATGGAAAGCATGACAATCTT
TTGGGCTTTGCTTGAATTCTGTGAATGCATACATATAAGCTAAACAGATGTCTGCAGTTA

57895

TCCTGTGATGAGTATATTTGAGAATACATGCAATGCACTAGCAAGTTACAATTGATAGAA
TACATTTGAAATGTTAAATGAAATAAGCCAGGCACAGAAAGACAAACACCACATGATCTC
ACTCATATGTGGAAATTTAAAAAGTTGATCTCACTCATATGTGGAAATTTAAAAAGTTGA
TCTCACACAAGTAGAGGCTAGAATCGTGGTTACGAGGGGCTAGGGAGAGAAAGAAGGCAG
AGGCACTGAAAGATGTTGGTCAATGGGTATAAAGTTACACCTAGGAAGAATAAATTTTGG
[C, T]

ATTCACCACAGTAGGGTGACTATAGCAAATAATAATGTAGCATGTATTTCAAGATAGCTA
GAAAAGCAGGTTTTTAAATGTCACCACAAAGAAATAACAAATGTTTATAGTGGTGGATAT
GGTAATTACGCCCTATTTGATCATTATACTGTGTGTACATGCATTGAAACACCACATTGTA
TCCCATATATATGTACAATTATGTGCCCATTATACATTTAAAAAATAAATTTTAAAAACC
TTCAATTAACCTCTTGGTTTTAAAGAAAAATATAAACCAAACTACATGATCTCTAAAAACA